

M. Membership

16C1 Page 1 of 1
1652
#12 OIPE
LB
11/15/01

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/710,339

DATE: 06/07/2001
TIME: 12:20:27

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NOV 13 2001

TECH CENTER 1600/2900

3 <110> APPLICANT: Bisgard-Frantzen, Henrik
4 Pedersen, Sven
5 Svendsen, Allan
7 <120> TITLE OF INVENTION: Fungamyl-like Alpha-Amylase Variants
9 <130> FILE REFERENCE: 5835.200-US
11 <140> CURRENT APPLICATION NUMBER: US 09/710,339
12 <141> CURRENT FILING DATE: 2000-11-09
14 <150> PRIOR APPLICATION NUMBER: US 60/165,786
15 <151> PRIOR FILING DATE: 1999-11-16
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1734
23 <212> TYPE: DNA
24 <213> ORGANISM: Aspergillus Oryzae
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (54)..(1547)
29 <223> OTHER INFORMATION: mat_peptide
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35 1
36 104
37 gtc gcg tgg tgg tct cta ttt ctg tac ggc ctt cag gtc gcg gca cct
38 Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala Pro 15
39 5
40 10
41 gct ttg gct gca acg cct gcg gac tgg cga tgc caa tcc att tat ttc 152
42 Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe 30
43 20 25
44 200
45 ctt ctc acg gat cga ttt gca agg acg gat ggg tgc acg act gcg act
46 Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr 45
47 35 40
48 248
49 tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc
50 Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile 65
51 50 55
52 296
53 atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg
54 Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp 80
55 70
56 344
57 atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat
58 Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp 95
59 85 90
60 392
61 gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac
62 Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn 110
63 100 105
64 440
65 tac ggc act gca gat gac ttg aag gcg ctc tct tgc gcc ctt cat gag
66 Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu 125
67 115 120

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69	agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat	488
70	Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr	
71	130 135 140 145	
73	gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt	536
74	Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser	
75	150 155 160	
77	tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat	584
78	Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp	
79	165 170 175	
81	cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg	632
82	Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu	
83	180 185 190	
85	cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac	680
86	Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp	
87	195 200 205	
89	tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt atc	728
90	Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile	
91	210 215 220 225	
93	gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa	776
94	Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys	
95	230 235 240	
97	gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc	824
98	Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala	
99	245 250 255	
101	tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc	872
102	Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro	
103	260 265 270	
105	att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg	920
106	Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met	
107	275 280 285	
109	gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac	968
110	Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp	
111	290 295 300 305	
113	tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc	1016
114	Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe	
115	310 315 320	
117	gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc	1064
118	Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe	
119	325 330 335	
121	atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag	1112
122	Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln	
123	340 345 350	
125	cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc	1160
126	His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu	
127	355 360 365	
129	tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg	1208
130	Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala	
131	370 375 380 385	
133	aac gca atc ccg aac tat gcc att agc aaa gat aca gga ttc gtg acc	1256

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137 tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc      1304
138 Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg
139                               405                               410                               415
141 aag ggc aca gat ggg tgc cag atc gtg act atc ttg tcc aac aag ggt      1352
142 Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly
143                               420                               425                               430
145 gct tgc ggt gat tgc tat acc ctc tcc ttg agt ggt gcg ggt tac aca      1400
146 Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr
147                               435                               440                               445
149 gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt      1448
150 Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val
151 450                               455                               460                               465
153 ggt tgc gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg      1496
154 Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg
155                               470                               475                               480
157 gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt agc      1544
158 Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser
159                               485                               490                               495
161 tgc tgaaggggtg agagtatatg atggtactgc tattcaatct ggcattggac      1597
162 Ser
165 agtgagtttg agtttgatgt acagttggag tcgttactgc tgtcatcccc ttatactctt      1657
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174 <212> TYPE: PRT
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184                               20                               25                               30
187 Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
188                               35                               40                               45
191 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
192 50                               55                               60
195 Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
196 65                               70                               75                               80
199 Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
200                               85                               90                               95
203 Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
204                               100                              105                              110
207 Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
208                               115                              120                              125
211 Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
212 130                               135                               140
215 Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe

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216 145
219 Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
220 165 170 175
223 Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
224 180 185 190
227 Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
228 195 200 205
231 Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
232 210 215 220
235 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
236 225 230 235 240
239 Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
240 245 250 255
243 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
244 260 265 270
247 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
248 275 280 285
251 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
252 290 295 300
255 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
256 305 310 315 320
259 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
260 325 330 335
263 Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
264 340 345 350
267 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
268 355 360 365
271 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
272 370 375 380
275 Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
276 385 390 395 400
279 Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
280 405 410 415
283 Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
284 420 425 430
287 Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
288 435 440 445
291 Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
292 450 455 460
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303 Ser Ser
307 <210> SEQ ID NO: 3
308 <211> LENGTH: 498
309 <212> TYPE: PRT
310 <213> ORGANISM: Aspergillus oryzae
312 <400> SEQUENCE: 3

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314 Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala
315 1 5 10 15
317 Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
318 20 25 30
320 Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
321 35 40 45
323 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
324 50 55 60
326 Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
327 65 70 75 80
329 Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
330 85 90 95
332 Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
333 100 105 110
335 Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
336 115 120 125
338 Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
339 130 135 140
341 Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
342 145 150 155 160
344 Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
345 165 170 175
347 Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
348 180 185 190
350 Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
351 195 200 205
353 Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
354 210 215 220
356 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
357 225 230 235 240
359 Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
360 245 250 255
362 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
363 260 265 270
365 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
366 275 280 285
368 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
369 290 295 300
371 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
372 305 310 315 320
374 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
375 325 330 335
377 Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
378 340 345 350
380 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
381 355 360 365
383 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
384 370 375 380
386 Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val

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VERIFICATION SUMMARY

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Input Set : A:\5835.ST25.txt

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